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A3

WO 01/87982

(54) Title: IMMUNOTOXIN FUSION PROTEINS AND MEANS FOR EXPRESSION THEREOF

(57) Abstract: The present invention described and shown in the specification and drawings provides novel recombinant DT-based immunotoxins, and, more specifically anti-T cell immunotoxin fusion proteins. Also provided are immunotoxins that can be expressed in bacterial, yeast, or mammalian cells. The invention also provides means for expression of the immunotoxin fusion protein. It is emphasized that this abstract is provided to comply with the rules requiring an abstract that will allow a searcher or other reader to quickly ascertain the subject matter of the technical disclosure. It is submitted with the understanding that it will not be used to interpret or limit the scope or meaning of the claims.

INTERNATIONAL SEARCH REPORT

Int'l Application No
PCT/US 01/16125

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/62 C07K19/00 C12N15/63 C12N1/19 C12N1/21
C12N5/10 //C07K16/28, C07K14/34

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EMBASE, CHEM ABS Data, WPI Data, PAJ, EPO-Internal, SEQUENCE SEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 39363 A (THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES ET AL.) 11 September 1998 (1998-09-11) examples 8-10 claims figures 11,14	1,15-26, 29,30, 33-41, 45, 54-67, 79,80, 92-97, 116-119
Y	---	31,32, 43,44, 77,78, 99-103 -/-



Further documents are listed in the continuation of box C



Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
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- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *&* document member of the same patent family

Date of the actual completion of the international search

26 November 2001

Date of mailing of the international search report

10/12/2001

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INTERNATIONAL SEARCH REPORT

Int'l Application No

PCT/US 01/16125

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 98 39425 A (THE SECRETARY, THE DEPARTMENT OF HEALTH AND HUMAN SERVICES) 11 September 1998 (1998-09-11) the whole document ---	31, 32, 43, 44, 77, 78, 99-103
X	WO 96 32137 A (THE SECRETARY, THE DEPARTMENT OF HEALTH AND HUMAN SERVICES ET AL.) 17 October 1996 (1996-10-17) examples 9-11 claims 1, 22, 23 ---	1, 15-26, 29, 30, 33-41, 45, 54-67, 79, 80, 92-97, 116-119
X	J. THOMPSON ET AL.: "An anti-CD3 single-chain immunotoxin with a truncated diphtheria toxin avoids inhibition by pre-existing antibodies in human blood." THE JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 270, no. 47, 24 November 1995 (1995-11-24), pages 28037-28041, XP002083389 Baltimore, MD, USA the whole document	1, 15-26, 33-40, 116-119
Y		29, 30, 41, 43-45, 54-67, 79, 80, 92-97, 101, 102
Y	S. MA ET AL.: "Expression and characterization of a divalent chimeric anti-human CD3 single-chain antibody." SCANDINAVIAN JOURNAL OF IMMUNOLOGY, vol. 43, no. 2, February 1996 (1996-02), pages 134-139, XP002083387 Oxford, GB the whole document ---	29, 30, 41, 45, 54-67, 79, 80, 92-97
Y	M. KIEKE ET AL.: "Isolation of anti-T cell receptor scFv mutants by yeast surface display." PROTEIN ENGINEERING, vol. 10, no. 11, 1997, pages 1303-1310, XP002064403 Oxford, GB abstract ---	43, 44, 101, 102
		-/-

INTERNATIONAL SEARCH REPORT

Int'l Application No

PCT/US 01/16125

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication where appropriate, of the relevant passages	Relevant to claim No.
A	<p>D. VALLERA ET AL.: "Anti-graft-versus-host disease effect of DT390-anti-CD3sFv, a single-chain Fv fusion immunotoxin specifically targeting the CD3-epsilon moiety of the T-cell receptor." BLOOD, vol. 88, no. 6, 15 September 1996 (1996-09-15), pages 2342-2353, XP000645998 Philadelphia, PA, USA the whole document</p> <p>---</p> <p>S. MA ET AL.: "Genetic construction and characterization of an anti-monkey CD3 single-chain immunotoxin with a truncated diphtheria toxin." BIOCONJUGATE CHEMISTRY, vol. 8, no. 5, September 1997 (1997-09), pages 695-701. XP002183986 Washington, DC, USA abstract</p> <p>-----</p>	1, 15-26, 33-40, 116-119
A		1, 15-26, 33-40, 116-119

INTERNATIONAL SEARCH REPORT

Information on patent family members

In' ational Application No

PCT/US 01/16125

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 9839363	A	11-09-1998	AU	733898 B2	31-05-2001
			AU	6542698 A	22-09-1998
			EP	1015496 A2	05-07-2000
			WO	9839363 A2	11-09-1998
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			AU	6445998 A	22-09-1998
			EP	0968282 A2	05-01-2000
			WO	9839425 A2	11-09-1998
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			CA	2218166 A1	17-10-1996
			EP	0830146 A2	25-03-1998
			WO	9632137 A2	17-10-1996
			US	5762927 A	09-06-1998

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35 40 45
Asp Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala
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Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly
 65 70 75 80
 Val Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys
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 Val Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr
 100 105 110
 Glu Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe
 115 120 125
 Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly
 130 135 140
 Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu
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 Ser Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln
 165 170 175
 Asp Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val
 180 185 190
 Arg Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp
 195 200 205
 Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His
 210 215 220
 Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Ala Lys Thr Val Ser
 225 230 235 240
 Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu
 245 250 255
 Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro
 260 265 270
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 Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val
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 370 375 380
 His Lys Thr Gln Pro Phe Leu Pro Trp Asp Ile Gln Met Thr Gln Thr
 385 390 395 400
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 405 410 415
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 690 695 700
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 755 760 765
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 770 775 780
 Leu Val Lys Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala Ser Gly
 785 790 795 800
 Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly
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 835 840 845
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 850 855 860

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synthetic construct

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 35 40 45
 Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala Gly
 50 55 60
 Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val
 65 70 75 80
 Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val
 85 90 95
 Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
 100 105 110
 Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly
 115 120 125
 Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser
 130 135 140
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 145 150 155 160
 Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp
 165 170 175
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 195 200 205
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 50 55 60
 Asp Ala Ala Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys
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 245 250 255
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 260 265 270
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 340 345 350
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 450 455 460
 Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala
 465 470 475 480
 Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly
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Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp
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Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly	Asp
							660					665			670
Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Arg	Asn	Tyr	Leu
							675					680			685
Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gly	Thr	Val	Lys	Leu	Leu	Ile	Tyr
							690					695			700
Tyr	Thr	Ser	Arg	Leu	His	Ser	Gly	Val	Pro	Ser	Lys	Phe	Ser	Gly	Ser
705							710					715			720
Gly	Ser	Gly	Thr	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Gln	Glu
							725					730			735
Asp	Ile	Ala	Thr	Phe	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Trp	Thr	
							740					745			750
Phe	Ala	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Gly	Ser	Gly		
							755					760			765
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Gln	Gln	Ser
							770					775			780
Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	Met	Lys	Ile	Ser	Cys	Lys
785							790					795			800
Ala	Ser	Gly	Tyr	Ser	Phe	Thr	Gly	Tyr	Thr	Met	Asn	Trp	Val	Lys	Gln
							805					810			815
Ser	His	Gly	Lys	Asn	Leu	Glu	Trp	Met	Gly	Leu	Ile	Asn	Pro	Tyr	Lys
							820					825			830
Gly	Val	Ser	Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr
							835					840			845
Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Leu	Ser	Leu	Thr
							850					855			860
Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Gly	Tyr	Tyr	Gly
865							870					875			880
Asp	Ser	Asp	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr
							885					890			895
Val	Phe	Ser													

<210> 29

<211> 89

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =

synthetic construct

<400> 29

Met	Arg	Phe	Pro	Ser	Ile	Phe	Thr	Ala	Val	Leu	Phe	Ala	Ala	Ser	Ser
1									10					15	

Ala	Leu	Ala	Ala	Pro	Cys	Asn	Thr	Thr	Glu	Asp	Glu	Thr	Ala	Gln	
							20	25				30			
Ile	Pro	Ala	Glu	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe
							35	40				45			
Asp	Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu
							50	55				60			
Phe	Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Glu	Gly	Val
							65	70				75		80	
Ser	Leu	Glu	Lys	Arg	Glu	Ala	Glu	Ala							
							85								

<210> 30

<211> 2952

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 30

atgagatttc	cttcaatttt	tactgctgtt	ttattcgacg	cattcctccgc	attagctgct	60
ccagtcaaca	ctacaacaga	agatgaaacg	gcacaaattc	cgctgaagg	tgtcatcggt	120
tactcgatt	tagaagggga	tttcgatgtt	gtgttttgc	cattttccaa	cagcacaat	180
aacgggttat	tgtttataaa	tactacttt	gccagcattt	ctgcttaaga	agaagggtt	240
tctctcgaga	aaagagctgg	cgctgatgt	gtcgtcgact	cctccaagtc	cttcgtcatg	300
gagaacttcg	cttcctacc	cgggaccaag	ccaggttacg	tcgactccat	ccagaagggt	360
atccagaagc	caaagtccgg	cacccaaagg	aactacgacg	acgactggaa	ggggttctac	420
tccaccgaca	acaagtagca	cgctcgaaa	tactctgttg	ataatgaaaa	cccgctctct	480
ggaaaagctg	gaggcgttgt	caaagtgacg	tatccaggac	tgacgaagg	tctcgacta	540
aaagtggata	atgcccac	tattaagaaa	gagttagg	taagtctcac	tgaaccgttg	600
atggagcaag	tccgaaacgg	agagtttac	aaaaggttgc	gtgatggtgc	ttcgcgtgt	660
gtgctcagcc	ttcccttcgc	tgagggag	tctagcggt	aatatattaa	taactggaa	720
caggcgaaag	cgtaaggcgt	agaacttgg	attaatttt	aaaccctgtgg	aaaacgtggc	780
caagatgcga	tgtatgagta	tatggctaa	gcctgtgcag	gaaatcgtgt	caggcgatca	840
gttaggtagct	cattgtcatg	cataaatctt	gattggatg	tcataaggaa	taaaaactaag	900
acaaagatag	agtctttgaa	agagcatggc	ccaatcaaga	acaagatgtc	cgaatcccc	960
gctaagaccg	tctccgagga	aaaggccaag	caatacctag	aagagttcca	ccaaaccgccc	1020
ttggagcatac	ctgaattgtc	agaacttaaa	accgttact	ggaccaatcc	tgtattcgct	1080
ggggctaact	atgcggcgtg	ggcagtaaac	tttgcgcag	ttatcgatag	cgaaacagct	1140
gataattttgg	aaaagacaaac	tgctgtctt	tcgataact	ctggatcgg	tagcgtatg	1200
ggcattcgag	acgggtccgt	tcaccacaa	acagaagaga	tagtggcaca	atccatcgct	1260
ttgtcccttt	tgtatggttg	tcaagatc	ccattggtgc	gtgatgggt	tgacatcggt	1320
ttcgcgtcct	acaacttcgt	cgagtccatc	atcaacttgt	tccaaatcg	ccacaactcc	1380
tacaaccgtc	cggttactc	cccaggta	aagacccaa	cattttgc	atgggacatc	1440
cagatgaccc	agaccaccc	ctccctgtct	gcctccctgg	gcgacagagt	caccatcagt	1500
tgcaggcaca	gtcaggacat	tagaaattat	ttaaaactgg	atcaacagaa	accagatgga	1560
actgttaaac	tcctgtatca	ctacacatca	agattacact	caggagtccc	atcaaagttc	1620
agtggcagtg	ggtctggaa	agattattct	ctcaccat	gcaacctgg	gcaaggaggat	1680
attgcccatt	acttttgcc	acagggtaat	acgcttcgt	ggacgttcgc	tggaggcacc	1740
aagctggaga	taaaaggagg	cgaggcagc	ggaggcggt	gctcgggagg	gggaggctcg	1800
gaggtgcagc	tccagcagtc	tggacctgg	ctggtgaagc	ctggagcttc	aatgaagata	1860
tcctgcaagg	cttctgggtt	ctcattact	ggctacacca	tgaactgggt	gaagcagagt	1920
catggaaaga	accttgagt	gatgggactt	attaatcctt	acaaagggtgt	tagtacctac	1980
aaccagaagt	tcaaggacaa	ggccacatta	actgttagaca	agtcatccag	cacaggctac	2040
atggaactcc	tcaagtctgac	atctgaggac	tctgcagtc	attactgtgc	aagatcgcccc	2100

tactacggtg atagtgactg gtacttcgat	gtctggggcg cagggcaccac tgcacagtc	2160
tcctcaggag gtggcggatc cgaggaggc	ggtagtggcg gaggcggttc ggacatccag	2220
atgacccaga ccacctcc tcgtctgc	tcctggcg acagagtcac catcaatgc	2280
agggcaagtc aggacattag aaattat	aactggatc aacagaaacc agatgaaact	2340
gttaaactcc tgatctacta cacatcaaga	ttacactcag gagtcccata aaagttcagt	2400
ggcagtgggt ctggaacaga ttattctctc	accattagca acctggagca agaggatatt	2460
gccacttact tttgccaaca gggtaatacg	cttccgtgga cttcgtctgg aggcccaag	2520
ctggagataa aaggaggcgg aggagcgg	ggcggtggtc cgggaggggg aggctcggag	2580
gtgcagctcc agcagtctgg acctgagctg	gtgaaggctg gagcttcaat gaagatatcc	2640
tgcaaggctt ctggttactc attactggc	tacaccatga actgggtgaa gcagagtcat	2700
ggaaagaacc ttgagtggat gggacttatt	aatccttaca aaggtgttag tacctacaac	2760
cagaagttca aggacaaggc cacattaact	gtagacaagt catccagcac agcctacatg	2820
gaactcctca gtctgacatc tgaggactct	gcagtcattt actgtgcaag atcgggtac	2880
tacggtgata gtgactggta cttcgatgtc	tggggccaag gcaccactct cacagtcttc	2940
tcatgagaat tc		2952

<210> 31

<211> 85

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 31

Met	Arg	Phe	Pro	Ser	Ile	Phe	Thr	Ala	Val	Leu	Phe	Ala	Ala	Ser	Ser
1					5				10					15	
Ala	Leu	Ala	Ala	Pro	Cys	Asn	Thr	Thr	Thr	Glu	Asp	Glu	Thr	Ala	Gln
								20	25					30	
Ile	Pro	Ala	Glu	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe
								35	40					45	
Asp	Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu
								50	55					60	
Phe	Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Gly	Val	
								65	70					80	
Ser	Leu	Glu	Lys	Arg											
					85										

<210> 32

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<400> 32

Ala	Ile	His	Arg	Gly	Gly	Gly
1				5		

<210> 33

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 33

gccccatccacc gaggaggtgg t

<210> 34

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 34

Met Gly Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ala Asp Ala Ala
20

<210> 35

<211> 210

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 35

gttcaccaca atacagaaga gatagtggca caatccatcg ctttgcctc tttgatggtt 60
gctcaagcta tcccattgtt cggtgagttg gttgacatcg gtttcgctgc ctacaacttc 120
gtcgagtcca tcatacaactt gttccaagtc gtccacaact cctacaaccg tccggcttac 180
tccccaggtc acaagaccca accattcttg 210

<210> 36

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 36

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

Arg Gly Ser His Met
20

<210> 37

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<400> 37

Ala Ser Ala Gly Gly Ser
1 5

<210> 38

<211> 642

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 38
Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu Asn
1 5 10 15
Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile Gln
20 25 30
Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp Asp
35 40 45
Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala Gly
50 55 60
Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val
65 70 75 80
Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val
85 90 95
Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
100 105 110
Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly
115 120 125
Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser
130 135 140
Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser
145 150 155 160
Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp
165 170 175
Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val Arg
180 185 190
Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val
195 200 205
Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly
210 215 220
Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu
225 230 235 240
Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu
245 250 255
His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro Val
260 265 270
Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val
275 280 285
Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu
290 295 300
Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala
305 310 315 320
Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser
325 330 335
Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp
340 345 350
Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu Phe
355 360 365
Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly His
370 375 380
Lys Thr Gln Pro Phe Ala Ser Ala Gly Gly Ser Asp Ile Gln Met Thr
385 390 395 400
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
405 410 415
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
420 425 430
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
435 440 445

Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr
 450 455 460
 Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr
 465 470 475 480
 Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly Gly
 485 490 495
 Thr Lys Leu Glu Ile Lys Arg Ala Gly Gly Ser Gly Gly Ser
 500 505 510
 Gly Gly Ser Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly
 515 520 525
 Pro Glu Leu Val Lys Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala
 530 535 540
 Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser
 545 550 555 560
 His Gly Lys Asn Leu Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly
 565 570 575
 Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Val
 580 585 590
 Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser
 595 600 605
 Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp
 610 615 620
 Ser Asp Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val
 625 630 635 640
 Ser Ser

<210> 39
 <211> 656
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 39
 Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro Arg
 1 5 10 15
 Gly Ser His Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val
 20 25 30
 Met Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp
 35 40 45
 Ser Ile Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn
 50 55 60
 Tyr Asp Asp Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp
 65 70 75 80
 Ala Ala Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala
 85 90 95
 Gly Gly Val Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala
 100 105 110
 Leu Lys Val Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser
 115 120 125
 Leu Thr Glu Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys
 130 135 140
 Arg Phe Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala
 145 150 155 160
 Glu Gly Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys
 165 170 175
 Ala Leu Ser Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg
 180 185 190

Gly Gln Asp Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn
 195 200 205
 Arg Val Arg Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp
 210 215 220
 Trp Asp Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys
 225 230 235 240
 Glu His Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr
 245 250 255
 Val Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr
 260 265 270
 Ala Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr
 275 280 285
 Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val
 290 295 300
 Ala Gln Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr
 305 310 315 320
 Ala Ala Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala
 325 330 335
 Asp Gly Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile
 340 345 350
 Ala Leu Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu
 355 360 365
 Leu Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile
 370 375 380
 Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser
 385 390 395 400
 Pro Gly His Lys Thr Gln Pro Phe Leu Pro Trp Asp Ile Gln Met Thr
 405 410 415
 Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
 420 425 430
 Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
 435 440 445
 Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
 450 455 460
 Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr
 465 470 475 480
 Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr
 485 490 495
 Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly Gly
 500 505 510
 Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly Gly
 515 520 525
 Ser Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
 530 535 540
 Leu Val Lys Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala Ser Gly
 545 550 555 560
 Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly
 565 570 575
 Lys Asn Leu Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser
 580 585 590
 Thr Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Phe Thr Val Asp Lys
 595 600 605
 Ser Ser Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp
 610 615 620
 Ser Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp
 625 630 635 640
 Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Leu Thr Val Phe Ser
 645 650 655

<210> 40
 <211> 1943
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 40

ccatgggcgc tcatgtatgtt gttgattctt ctaaatctt ttttatggaa aactttctt	60
cgtaccacgg gactaaacct gtttatgtat ttccattca aaaaggata caaaagccaa	120
aatcttgtat gttttatgtat atggaaagg gttttatagt accgacaata	180
aatacgcgc tgcgggatata tctgtatata atggaaaacc gctctctgaa aaagctggag	240
gcgtggatca aatgtatgtat ccaggactga cgaaggatct cgcactaaaa gtggataatg	300
ccgaaaactat taagaaagag ttatgtttaa gtctactga accgttgatg gagcaagtgc	360
gaacgaaaga gtttatcaaa aggttcggtg atgggtcttc gctgttagt ctcagccccc	420
ccttcgtat ggggatctt acgtttgtat atattaataa ctgggaaacag gcgaaagcgt	480
taagcgatata acttgatgat aatttgtaaa cccgtggaaa acgtggccaa gatgcgtat	540
atagatataat ggctcaagcc tttgcaggaa atcgtgtatc gcgatcagta ggtatgtat	600
tgtcatgtat aatcttgc tggatgtca taaggatataa aactaagaca aagatagat	660
cattttgaaaga gcatggccct atcaaaaataa aatgagcga aagtcccaat aaaacagtat	720
ctgaggaaaa agctaaacaa tacatgaaag aattgtcaga acttaaaacc gttactggaa	780
ccaaatccgtt attcgctggg gctaactatg tcgatagcga aacagctgat aatttggaaa	840
gtatcggtat cgtatgggc attgcagacg tggcacaatc aatagcttta tcgtctttaa	900
agctatgtatc tatttttttc gctgcataata aagtatgtca taattcgat aatcgcccc	960
ttgctccgc cggggatcc gacatccaga ctctgggaga cagagtacc atcagttca	1020
ggggcaatca gggatccatc acatcaatggat aatattttaa actgtatca acagaaacca gatggaaactg	1080
ttaaactctt gatctactac acatcaatggat gcaatgttca gtttactcatc aatcttgc	1140
ttttttttttt gggggatccatc acgtttttttt gttttttttt gttttttttt gttttttttt	1200
ttgatccatc acatcaatggat gggatccatc acatcaatggat gggatccatc acatcaatggat	1260
ttttttttttt gggggatccatc acatcaatggat gggatccatc acatcaatggat gggatccatc acatcaatggat	1320
ttttttttttt gggggatccatc acatcaatggat gggatccatc acatcaatggat gggatccatc acatcaatggat	1380
ttttttttttt gggggatccatc acatcaatggat gggatccatc acatcaatggat gggatccatc acatcaatggat	1440
ttttttttttt gggggatccatc acatcaatggat gggatccatc acatcaatggat gggatccatc acatcaatggat	1500
ttttttttttt gggggatccatc acatcaatggat gggatccatc acatcaatggat gggatccatc acatcaatggat	1560
ttttttttttt gggggatccatc acatcaatggat gggatccatc acatcaatggat gggatccatc acatcaatggat	1620
ttttttttttt gggggatccatc acatcaatggat gggatccatc acatcaatggat gggatccatc acatcaatggat	1680
ttttttttttt gggggatccatc acatcaatggat gggatccatc acatcaatggat gggatccatc acatcaatggat	1740
ttttttttttt gggggatccatc acatcaatggat gggatccatc acatcaatggat gggatccatc acatcaatggat	1800
ttttttttttt gggggatccatc acatcaatggat gggatccatc acatcaatggat gggatccatc acatcaatggat	1860
ttttttttttt gggggatccatc acatcaatggat gggatccatc acatcaatggat gggatccatc acatcaatggat	1920
ttttttttttt gggggatccatc acatcaatggat gggatccatc acatcaatggat gggatccatc acatcaatggat	1943

<210> 41

<211> 1940

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 41

tggcgctga tcatgtatgtt gtttcttctt aatctttgtt gatggaaaac ttttcttcgt	60
accacggggac taaaacctgtt tatgtatgtt ccattcaaaa aggtatacaa aagccaaaat	120
ctggcacaca aggaaattat gacgtatgtt ggaaagggtt ttatgtatgtt gacaataat	180
acgacgctgc gggatactct gtatgtatgtt aaaacccgtt ctctggaaaa gctggaggcg	240
tggtcaaagt gacgtatgtt ggactgtatgtt aggttctcgc actaaaatgt gataatgcgc	300
aaactattaa gaaagatgtt gttttaatgtt tcactgtatgtt gtttgcgtatgtt caagtccggaa	360
cggaagatgtt tatcaaaaagg ttcggatgtt gtgttctcgc tttttttttt tttttttttt	420
tcgctgatggg gagttctatgtt gttttaatgtt ttaataatgtt ggaacaggcg aaagctttaa	480
gcgtatgtatgtt tttttttttt gtttgcgtatgtt gtttgcgtatgtt gtttgcgtatgtt gtttgcgtatgtt	540
agtatgtatgtt tttttttttt gtttgcgtatgtt gtttgcgtatgtt gtttgcgtatgtt gtttgcgtatgtt	600
catgcataaaa tttttttttt gtttgcgtatgtt gtttgcgtatgtt gtttgcgtatgtt gtttgcgtatgtt	660

tgaaagagca	tggccctatc	aaaaataaaa	tgagcgaaag	tcccaataaa	acagtatctg	720
aggaaaaaggc	taaacaatac	ctagaagaat	ttcatcaaac	ggcatttagag	catcctgaat	780
tgtcagaact	taaaaccgtt	actgggacca	atcctgtatt	cgctggggct	aactatgcgg	840
cgtggcagt	aaacgttgcg	caagttatcg	atagcgaaac	agctgataat	ttggaaaaga	900
caactgctgc	tcttcgata	cttctggta	tcggtagcgt	aatgggcatt	gcagacggtg	960
ccggtcacca	caatacagaa	gagatagtgg	cacaatcaat	agctttatcg	tctttaatgg	1020
ttgctcaagc	tattccattg	gttaggagac	tagttgat	tggtttcgct	gcatataatt	1080
ttgttagagag	tattatcaat	ttatttcaag	tagttcataa	ttcgtataat	cgtccgcgt	1140
attctccggg	gcataaaaacg	caaccatttg	cttccggcg	tggatccgac	atccagatga	1200
cccagaccac	ctcctccctg	tctgcctctc	tggagacag	agtaccatc	agttgcaggg	1260
caagtcaagg	cattagaaat	tattaaact	ggtatcaaca	gaaaccagat	ggaactgtta	1320
aactcctgtat	ctactacaca	tcaagattac	actcaggagt	cccatcaaag	ttcagtggca	1380
gtgggtctgg	aacagattat	tcttcacca	ttagcaacct	ggagcaagag	gatattgcca	1440
cttacttttg	ccaacagggt	aatacgttc	cgtggacgtt	cgctggaggc	accaagctgg	1500
aatcaaaccg	ggctggaggc	ggttagtggcg	gtggatcagg	tggaggcagc	ggtggcggat	1560
ctgagggtca	gctccagcag	tctggacctg	agctggtaa	gcctggagct	tcaatgaaga	1620
tatcctgcaa	gcttctgtt	tactcattca	ctggctacac	catgaactgg	gtgaagcaga	1680
gtcatggaaa	gaaccctttag	tggatgggac	ttattaatcc	ttacaaaggt	gttagtacct	1740
acaaccagaa	gttcaaggac	aaggccacat	taactgtaga	caagtcatcc	agcacacgcot	1800
acatgaaact	cctcagtctg	acatctgagg	actctgcagt	ctattactgt	gcaagatcgg	1860
ggtactacgg	tgatagttgac	tggtaacttcg	atgtctgggg	cgcagggacc	acggtcaccg	1920
tctcctcatg	atagagatct					1940

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 42

Pro Gly Gly Asn Arg Gly Thr Thr Arg Pro Ala Thr Ser Gly Ser Ser
1 5 10 15Pro Gly Pro Thr Asn Ser His Tyr
20

<210> 43

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 43

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 44

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 44

cgggatccag tcgacatgga gacagacaca ctccctttat gggtaactgct gctctgggtt 60
cca 63

<210> 45
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 45
gtactgctgc tctgggttcc aggtgccgac gctgctggcg ctgatgatgt tgttgat 57

<210> 46
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 46
atagaattct tagtggtggt ggtggtggtg tgagaagact gtgagagtgg tgcctt 56

<210> 47
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 47
Glu Ala Glu Ala Tyr Val Glu Phe
1 5

<210> 48
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 48
Glu Ala Tyr Val Glu Phe
1 5

<210> 49
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 49
Tyr Val Glu Phe
1

<210> 50
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 50
tataccatgg gcgcgtatga ttttgttatg 30

<210> 51
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 51
actgcccacg ccgcatacg 23

<210> 52
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 52
ttgcgcacacg ttactgcc acgcgcata gtagccc 38

<210> 53
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 53
cgctatcgat aacttgcgca acgtttactg ccc 33

<210> 54
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 54
gcagttgtct ttccaaatt atcagctgtt tcgctatcga taac 44

<210> 55
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 55
gctaccgata ccaggaagta tcgaaagagc agcagttgtc ttttcc 46

<210> 56
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 56
gaacggcacc gtctgcaatg cccattacgc taccgatacc aggaagtatc gaaagag 57

<210> 57
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 57
actatatctt ctgtatttggtg gtgaacggca ccgtctgcaa tg 42

<210> 58
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 58
caaccattaa agacgataaa gctattgatt gtgccactat ctcttctg 48

<210> 59
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 59
ctacaaaatt atatgcagcg aaaccaatat caactagctc tcctaccaat ggaatagctt 60
gagcaaccat taaagacgt 80

<210> 60

<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 60
cgattatacg aattatgaac tacttcaaat aaattgataa tactctctac aaaatttat 60
gcagcgcg 66

<210> 61
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 61
gcgaatttcgg atccaccggc ggaagcaaat ggttgcgttt tatgccccgg agaatacg 60
ggacgattat acgaattatg aac 83

<210> 62
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 62
gcgaatttcgg atccaccggc ggaagcaaat ggttgcgttt tatgccccgg agaatacg 60
ggacgattat acgaattatg aac 83

<210> 63
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 63
aagttagttca taattcgtat aatcgtcccg cgtattctcc g 41

<210> 64
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 64
gcggatccga catccagatg acccagacca cc 32

<210> 65
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

 <400> 65

 cctctagaag cccgtttgat ttccagcttg gt 32

 <210> 66
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

 <400> 66
 ccgtcgacga ggtgcagctc cagcagtct 29

 <210> 67
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

 <400> 67
 ccaagtttc atgaggagac ggtgaccgtg gtccc 35

 <210> 68
 <211> 657
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

 <400> 68
 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15
 Arg Gly Ser His Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe
 20 25 30
 Val Met Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val
 35 40 45
 Asp Ser Ile Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly
 50 55 60
 Asn Tyr Asp Asp Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr
 65 70 75 80
 Asp Ala Ala Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys
 85 90 95
 Ala Gly Gly Val Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu
 100 105 110

Ala Leu Lys Val Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu
 115 120 125
 Ser Leu Thr Glu Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile
 130 135 140
 Lys Arg Phe Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe
 145 150 155 160
 Ala Glu Gly Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala
 165 170 175
 Lys Ala Leu Ser Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys
 180 185 190
 Arg Gly Gln Asp Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly
 195 200 205
 Asn Arg Val Arg Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu
 210 215 220
 Asp Trp Asp Val Ile Arg Asp Lys Thr Lys Thr Ile Glu Ser Leu
 225 230 235 240
 Lys Glu His Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys
 245 250 255
 Thr Val Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln
 260 265 270
 Thr Ala Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly
 275 280 285
 Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn
 290 295 300
 Val Ala Gln Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr
 305 310 315 320
 Thr Ala Ala Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile
 325 330 335
 Ala Asp Gly Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser
 340 345 350
 Ile Ala Leu Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly
 355 360 365
 Glu Leu Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile
 370 375 380
 Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr
 385 390 395 400
 Ser Pro Gly His Lys Thr Gln Pro Phe Leu Pro Trp Asp Ile Gln Met
 405 410 415
 Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr
 420 425 430
 Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr
 435 440 445
 Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser
 450 455 460
 Arg Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly
 465 470 475 480
 Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala
 485 490 495
 Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly
 500 505 510
 Gly Thr Lys Leu Glu Ile Lys Arg Gly Gly Ser Gly Gly Gly
 515 520 525
 Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro
 530 535 540
 Glu Leu Val Lys Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala Ser
 545 550 555 560
 Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His
 565 570 575
 Gly Lys Asn Leu Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly Val
 580 585 590
 Ser Thr Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Phe Thr Val Asp
 595 600 605

Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu
 610 615 620
 Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser
 625 630 635 640
 Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Leu Thr Val Phe
 645 650 655
 Ser

<210> 69
<211> 643
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 69
Met Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu
1 5 10 15
Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile
20 25 30
Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp
35 40 45
Asp Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala
50 55 60
Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly
65 70 75 80
Val Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys
85 90 95
Val Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr
100 105 110
Glu Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe
115 120 125
Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly
130 135 140
Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu
145 150 155 160
Ser Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln
165 170 175
Asp Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val
180 185 190
Arg Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp
195 200 205
Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His
210 215 220
Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser
225 230 235 240
Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu
245 250 255
Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro
260 265 270
Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln
275 280 285
Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala
290 295 300

Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly
 305 310 315 320
 Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu
 325 330 335
 Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val
 340 345 350
 Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu
 355 360 365
 Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly
 370 375 380
 His Lys Thr Gln Pro Phe Ala Ser Ala Gly Gly Ser Asp Ile Gln Met
 385 390 395 400
 Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr
 405 410 415
 Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr
 420 425 430
 Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser
 435 440 445
 Arg Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly
 450 455 460
 Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala
 465 470 475 480
 Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly
 485 490 495
 Gly Thr Lys Leu Glu Ile Lys Arg Ala Gly Gly Ser Gly Gly Gly
 500 505 510
 Ser Gly Gly Ser Gly Gly Ser Glu Val Gln Leu Gln Gln Ser
 515 520 525
 Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Met Lys Ile Ser Cys Lys
 530 535 540
 Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln
 545 550 555 560
 Ser His Gly Lys Asn Leu Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys
 565 570 575
 Gly Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr
 580 585 590
 Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr
 595 600 605
 Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly
 610 615 620
 Asp Ser Asp Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr
 625 630 635 640
 Val Ser Ser

<210> 70
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 70
 Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu
 1 5 10

<210> 71
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 71
atgagcgaaa gtcccaataa aacagtatct gaggaa 36

<210> 72
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 72
gagcgaagagt ccccagaaga cagtatctga gg 32

<210> 73
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 73
gaagacgaag ac 12

<210> 74
<211> 36
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 74
gtcttcgtct tcgtttcgtt ctgcgtttc gtcttc 36

<210> 75
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 75
Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu
1 5 10

<210> 76
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 76
atgagcgaaa gtcccaataa aacagtatct gaggaa

36

<210> 77
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 77
gagcgaagt ccggccaaaa cagtatctga gg

32

<210> 78
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 78
cggcca

6

<210> 79
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 79
tggccg

<210> 80
<211> 14
<212> PRT
<213> Artificial Sequence

6

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 80
Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu Lys Ala
1 5 10

<210> 81
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 81
atgagcgaaa gtcccaataa aacagtatct gagaaaaaac ct 42

<210> 82
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 82
gagcggaaagt cccaataaag cggtctctga ggaaaaacc 39

<210> 83
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 83
ggtctc 6

<210> 84
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 84
gagaccgaga ccgagaccga gaccgagacc 30

<210> 85
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 85
Ser Phe Val Met Glu Asn Phe Ser Ser Tyr His Gly
1 5 10

<210> 86
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 86
tcttttgtga tggaaaactt ttcttcgtac cacggg 36

<210> 87
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 87
cttttgtat ggaagctttt tcttcgtacc acg 33

<210> 88
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 88
aagctt 6

<210> 89
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 89
aagctt 6

<210> 90
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 90
Phe Val Met Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro
1 5 10

<210> 91
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 91
tttgtatgg aaaacttttc ttcgtaaccac gggactaaac ct 42

<210> 92
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 92
gtatggaaa actttgctag ctaccacggg actaaacc 38

<210> 93
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 93
gctagc 6

<210> 94
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

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<400> 94
gctagc                                         6

<210> 95
<211> 180
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 95
ggcgctgatg atgttgttga ttcttctaaa tcttttgta tgaaaaactt ttcttcgtac   60
cacgggacta aacctggta tgttagattcc attcaaaaag gtatacaaaa gccaaaatct   120
ggtacacaag gaaattatga cgatgattgg aaagggttt atagtaccga caataaatac   180

<210> 96
<211> 180
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 96
ggcgctgatg atgtcgtcga ctcctccaag tccttcgtca tggagaactt cgtttcctac   60
cacgggacca agccaggtta cgtcactcc atccagaagg gtatccagaa gccaaagtcc   120
ggcacccaag gtaactacga cgacgactgg aagggttct actccaccga caacaagtac   180

<210> 97
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 97
aaagagcatg gcccttatcaa aaataaaatg agcgaaagtc ccaataaaac agtatctgag   60
gaaaaagcta aacaataacct agaagaattt catcaaacgg cattagagca tcctgaattt   120

<210> 98
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
synthetic construct

<400> 98
aaagagcatg gcccaatcaa gaacaagatg tccgaatccc ccgcttaagac cgtctccgag   60
gaaaaggcca agcaataacct agaagagttc caccaaaccg cttggagca tcctgaattt   120

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<210> 99
 <211> 210
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 synthetic construct

<400> 99
 gttcaccaca atacagaaga gatagtggca caatcaatag ctttatcgctt ttaatggtt 60
 gctcaagcta ttccattgggt aggagagcta gttgatattt gtttcgctgc atataatttt 120
 gtagagagta ttatcaattt atttcaagta gttcataattt cgataatcg tcccgctat 180
 tctccggggc ataaaacgca accatttctt 210

<210> 100
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 100
 ccctgcacgc cgatgctatc cacagaagag gaggacaagt cattccaacc atgaag 56

<210> 101
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 101
 gccgatgcta tccacagaag a 21

<210> 102
 <211> 2691
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 102
 gctgggtctg acgacgtcg tgcactcctcc aagtccttcg tcattggagaa ctgcgttcc 60
 taccacggga ccaaggccagg ttacgtcgac tccatccaga aggttatcca gaaggccaaag 120
 tccggcaccc aaggtaacta cgacgacgac tggaaagggt tctactccac cgacaacaag 180
 tacgacgctg cgggataactc tgttagataat gaaaaccgc tctctggaaa agctggaggc 240
 gtggtaagg tcacacctcc aggtctgact aaggcttgg ctttgaaggt cgacaacgct 300
 gagaccatca agaaggagtt gggtttgtcc ttgactgagc cattgatgga gcaagtcggt 360
 accgaagagt tcatcaagag attcggtgac ggtgcttcca gagtcgttctt gtccttgcca 420
 ttcgctgagg gttttcttag cgttgaatat attaataact gggAACAGGC taaggctttg 480

tctgttgaat	tggagattaa	cttcgaaacc	agaggtaaga	gaggtaaga	tgcgatgtat	540
gagtatatgg	ctcaaggcctg	tgctggtaac	agagtacagc	ttctgttgg	ttcctcttig	600
tcctgtatca	accttagactg	ggacgtcatc	agagacaaga	ctaagaccaa	gatcgagtct	660
ttgaaaagac	atggcccaat	caagaacaag	atgtccgaat	cccccgctaa	gaccgtctcc	720
gaggaaaagg	ccaaggcaata	cctagaagag	ttccacccaa	ccgccttgg	gcatccctgaa	780
ttgtcagaac	ttaaacccgt	tactgggacc	aatccctgtat	tcgctggggc	taactatgctg	840
gcgtggcag	taaacgttgc	gcaagttatc	gatagcggaa	cagctgataa	tttgaaaag	900
acaactgctg	ctctttcgat	acttccctgg	atcggtagcg	taatgggcat	tgcagacgg	960
gccgttacc	acaatacaga	agagatgtg	gcacaatcca	tcgcttgc	ctctttgatg	1020
gttgctcaag	ctatcccatt	ggtcgggtgag	ttgggtgaca	tcggttgc	tgcctacaac	1080
ttcgtcagat	ccatcatcaa	cttggttccaa	gtcgtccaca	actcctacaa	ccgtccggct	1140
tactccccag	gtcacaagac	ccaaccattc	ttggccatgg	acatccagat	gaccaggacc	1200
acccctcccc	tgtctgcctc	cctggggcag	agagtcacca	tcagttgcag	ggcaagtca	1260
gacatcagaa	actacttggaa	ctgggtatcag	cagaagccag	acgtactgt	caagttttg	1320
atctactaca	cttccagatt	gcactctgg	gtcccatcta	agttctctgg	atctggttct	1380
ggtaactgact	actccttgcac	catctccaac	ttggagcaag	aggatattgc	cacttacttt	1440
tgccaacacgg	gtaatacgt	tcgggtggacg	ttcgctggag	gcaccaagtt	ggagatcaag	1500
ggtggaggag	gttctggagg	ttgtggatct	ggaggtggag	gttctgaggt	tcaattgcaa	1560
caatctggac	ctgagctgg	gaaggctgg	gcttcaatga	agatatcctg	caaggcttct	1620
ggttactcat	tcactggcta	caccatgaac	tgggtgaagc	agagtcatgg	aaagaacctt	1680
gagtggatgg	gtttgattaa	cccttacaag	ggtgtctcga	cctacaacca	gaagttcaag	1740
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ctgacatctg	aggactctgc	agtctattac	tgtgcaagat	cggggtacta	cggtgatagt	1860
gactggtaact	tcgatgtctg	gggtgctgg	actactgtca	ctgtctccctc	tggaggtgga	1920
ggatctggag	gagggtgg	ttgtgggtgg	ggtgtctgaca	tccagatgac	ccagaccacc	1980
tcctccctgt	ctgcctccct	gggcgacaga	gtcaccatca	gttgcagggo	aagtcaaggac	2040
atcagaaaact	acttgaactg	gtatcagcag	aagccagacg	gtactgtcaa	tttggatgtc	2100
tactacactt	ccagattgca	ctctgggtgc	ccatctaagt	tctctggatc	tgggtctgg	2160
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caacagggt	atacgcttcc	gtggacgtt	gctggagggca	ccaagttgg	gatcaagggt	2280
ggaggagggt	ctggagggtgg	ttggatctgg	ggtgagggtt	ctgagggtca	attgcaacaa	2340
tctggacctg	agctgggtgaa	gcctggagct	tcaatgaaga	tatcctgcaa	ggcttctgg	2400
tactcattca	ctggctacac	catgaactgg	gtgaagcaga	gtcatggaaa	gaaccttgg	2460
tggatgggtt	tgattaaccc	ttacaagggt	gtctcgac	acaaccagaa	gttcaaggac	2520
aaggctactt	tcactgtaga	caagtcatcc	agcacagcct	acatggaaact	cctcagtcg	2580
acatctgagg	actctgcagt	ctattactgt	gcaagatcgg	ggtactacgg	tgatagtgac	2640
tggtacttcg	atgtctgggg	tgctggtaact	actgtcactg	tctcctctta	a	2691

<210> 103

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 103

Met	Ser	Val	Pro	Thr	Gln	Val	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Thr
1					5				10				15		
Asp	Ala	Arg	Cys												
			20												

<210> 104

<211> 16

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 104
Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
1 5 10 15

<210> 105
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 105
Gly Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 106
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 106
Met Leu Ala Asp Asp
1 5

<210> 107
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 107
Met Leu Asp Asp
1

<210> 108
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 108
Ser Ala Asp Asp

1

<210> 109
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 109
Ser Pro Gly Ala Asp Asp
1 5

<210> 110
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 110
Gly Ala Asp Asp
1

<210> 111
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 111
Met Gly Ala Asp Asp
1 5

<210> 112
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 112
Met Ala Ala Asp Asp
1 5

<210> 113
<211> 4
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 113
Ala Ala Asp Asp
1

<210> 114
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 114
Met Ser Ala Asp Asp
1 5

<210> 115
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 115
Met Gly Ser Asp Asp
1 5

<210> 116
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 116
Met Gly Gly Asp Asp
1 5

<210> 117
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 117

Met Gly Val Asp Asp
1 5

<210> 118

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 118

Gly Gly Asp Asp
1

<210> 119

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 119

Gly Val Asp Asp
1

<210> 120

<211> 652

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 120

Ala	Gly	Ala	Asp	Asp	Val	Val	Asp	Ser	Ser	Lys	Ser	Phe	Val	Met	Glu
1					5			10						15	
Asn	Phe	Ala	Ser	Tyr	Mis	Gly	Thr	Lys	Pro	Gly	Tyr	Val	Asp	Ser	Ile
					20			25						30	
Gln	Lys	Gly	Ile	Gln	Lys	Pro	Lys	Ser	Gly	Thr	Gln	Gly	Asn	Tyr	Asp
					35			40				45			
Asp	Asp	Trp	Lys	Gly	Phe	Tyr	Ser	Thr	Asp	Asn	Lys	Tyr	Asp	Ala	Ala
					50			55			60				
Gly	Tyr	Ser	Val	Asp	Asn	Glu	Asn	Pro	Leu	Ser	Gly	Lys	Ala	Gly	Gly
					65			70			75			80	
Val	Val	Lys	Val	Thr	Tyr	Pro	Gly	Leu	Thr	Lys	Val	Leu	Ala	Leu	Lys
					85			90			95				
Val	Asp	Asn	Ala	Glu	Thr	Ile	Lys	Lys	Glu	Leu	Gly	Leu	Ser	Leu	Thr
					100			105			110				
Glu	Pro	Leu	Met	Glu	Gln	Val	Gly	Thr	Glu	Glu	Phe	Ile	Lys	Arg	Phe
					115			120			125				
Gly	Asp	Gly	Ala	Ser	Arg	Val	Val	Leu	Ser	Leu	Pro	Phe	Ala	Glu	Gly
					130			135			140				

Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gin Ala Lys Ala Leu
 145 150 155 160
 Ser Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln
 165 170 175
 Asp Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val
 180 185 190
 Arg Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp
 195 200 205
 Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His
 210 215 220
 Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Ala Lys Thr Val Ser
 225 230 235 240
 Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu
 245 250 255
 Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro
 260 265 270
 Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln
 275 280 285
 Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala
 290 295 300
 Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly
 305 310 315 320
 Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu
 325 330 335
 Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val
 340 345 350
 Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu
 355 360 365
 Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly
 370 375 380
 His Lys Thr Gln Pro Phe Leu Pro Trp Asp Ile Gln Met Thr Gln Thr
 385 390 395 400
 Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys
 405 410 415
 Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys
 420 425 430
 Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His
 435 440 445
 Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
 450 455 460
 Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe
 465 470 475 480
 Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly Gly Thr Lys
 485 490 495
 Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 500 505 510
 Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 515 520 525
 Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
 530 535 540
 Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu
 545 550 555 560
 Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn
 565 570 575
 Gln Lys Phe Lys Asp Lys Ala Thr Phe Thr Val Asp Lys Ser Ser Ser
 580 585 590
 Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val
 595 600 605

Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe
610 615 620
Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
625 630 635 640
Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser
645 650

<210> 121
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 121
Gly Gly Gly Ser Ser Gly Gly Ser Ser
1 5 10

<210> 122
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 122
Gly Ser Asp Asp
1